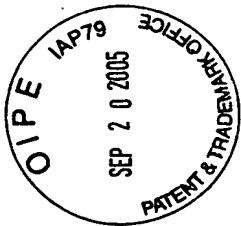


**Figure 1A**



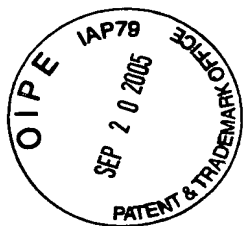
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 178 CGCCAATAGGGACTTTCCATTGACGTCAATGGGTGGACTATTTACGGTAAACTGCCAC  
 NdeI  
 237 TTGGCAGTACATCAAGTGTATCATATGCCAAGTACGCCCCCTATTGACGTCAATGACGG  
 CMV promotor  
 296 TAAATGGCCCGCCTGGCATTATGCCAGTACATGACCTTATGGGACTTTCCTACTTGGC  
 SnaBI  
 355 AGTACATCTACGTATTAGTCATCGCTATTACCATGGTGATGCGGTTTTGGCAGTACATC  
 414 AATGGGCGTGGATAGCGGTTTGACTCACGGGGATTTCCTCAAGTCTCCACCCCATGACGT  
 473 CAATGGGAGTTTGTGTTTGGCACCAAATCAACGGGACTTTCCTCAAAATGTCGTAACAACT  
 SacI  
 532 CCGCCCCATTGACGCAAATGGGCGGTAGGCGTGTACGGTGGGAGGTCTATATAAGCAGA  
 T7-Promotor  
 591 GCTCTCTGGCTAACTAGAGAACCCACTGCTTACTGGCTTATCGAAATTAATACGACTCA  
 Agel  
 HindIII KpnI  
 650 CTATAGGGAGACCCAAAGCTTGGTACCGGTGCGATGGCACCCCTGCATGCTGCTCCTGCTG  
 1►MetAlaProCysMetLeuLeuLeuLeu  
 SfiI NotI Apal EcoO109I  
 709 TTGGCGGGCGCCCTGGCCCCGACTCAGACCCGCGCGGGGGCCCAAAGGAGAAGACCCC  
 10►LeuAlaAlaLeuAlaProThrGlnThrArgAlaGlyAlaGlnLysGluLysThrPr  
 768 CGAGGAGCCCAAGGAGGAGGTGACCATCAAGGCCAACCTGATCTACGCCGACGGCAAGA  
 29►oGluGluProLysGluGluValThrIleLysAlaAsnLeuIleTyrAlaAspGlyLysT  
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 69►AlaAspAlaLeuLysLysAspAsnGlyGluTyrThrValAspValAlaAspLysGlyTy  
 945 CACCCTGAACATCAAGTTCGCCGGCAAGGAGAAGACCCCGAGGAGCCCAAGGAGGAGG  
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Figure 1 B(cont'd I)



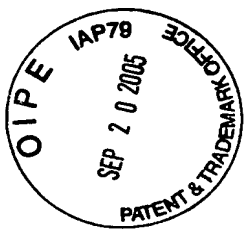
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1063 GGCACCTTCGAGGAGGCCACCGCGGAGGCCTACCGCTACGCCGACGCCCTGAAGAAGGA  
128▶ GlyThrPheGl uGl uAl aThrAl aGl uAl aTyrArgTyrAl aAspAl aLeuLysLysAs  
1122 CAACGGCGAGTACACCGTGGACGTGGCCGACAAGGGCTACACCCTGAACATCAAGTTTCG  
147▶ pAsnGlyGl uTyr Thr Val AspVal Al aAspLysGlyTyr Thr LeuAsn l l eLysPheA  
1181 CCGGCAAGGAGAAGACCCCCGAGGAGCCCAAGGAGGAGGTGACCATCAAGGCCAACCTG  
167▶ l aGlyLysGl uLysThr Pro Gl uGl uProLysGl uGl uVal Thr l l eLysAl aAsnLeu  
1240 ATCTACGCCGACGGCAAGACCCAGACCGCCGAGTTCAAGGGCACCTTCGAGGAGGCCAC  
187▶ l l eTyrAl aAspGlyLysThr Gl nThrAl aGl uPheLysGlyThrPheGl uGl uAl aTh  
1299 CGCGGAGGCCTACCGCTACGCCGACGCCCTGAAGAAGGACAACGGCGAGTACACCGTGG  
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1358 ACGTGGCCGACAAGGGCTACACCCTGAACATCAAGTTCCGCCGCAAGGAGAAGACCCCC  
226▶ spVal Al aAspLysGlyTyr Thr LeuAsn l l eLysPheAl aGl yLysGl uLysThr Pro  
  
1417 GAGGAGCCCCAAGGAGGAGGTGACCATCAAGGCCAACCTGATCTACGCCGACGGCAAGAC  
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1476 CCAGACCGCCGAGTTCAAGGGCACCTTCGAGGAGGCCACCGCGGAGGCCTACCGCTACG  
265▶ rGl nThrAl aGl uPheLysGlyThrPheGl uGl uAl aThrAl aGl uAl aTyrArgTyrA  
1535 CCGACGCCCTGAAGAAGGACAACGGCGAGTACACCGTGGACGTGGCCGACAAGGGCTAC  
285▶ l aAspAl aLeuLysLysAspAsnGlyGl uTyr Thr Val AspVal Al aAspLysGlyTyr  
SgrAl NotI  
1594 ACCCTGAACATCAAGTTCCGCCGGCGCGCCGCGAGCAACAAAACTCATCTCAGAAGAGGA  
305▶ ThrLeuAsn l l eLysPheAl aGl yAl aAl aAl aGl uGl nLysLeu l l eSer Gl uGl uAs  
  
Sall  
HincII  
AclI  
1653 TCTGAATGGGGCCGTCGACGGACAAAACGACACCAGCCAAACCAGCAGCCCCCTCAGCAT  
324▶ pLeuAsnGlyAl aVal AspGlyGl nAsnAspThr Ser Gl nThr Ser Ser ProSerAl aS  
  
MscI  
1712 CCAGCAACATAAGCGGAGGCATTTTCCTTTTCTTCGTGGCCAATGCCATAATCCACCTC  
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AflIII XbaI SacI  
1771 TTCTGCTTCAGTTGAGGTGACACGTCTAGAGCTATTCTATAGTGTCACCTAAATGCTAG  
364▶ PheCysPheSer •••  
  
BclI  
1830 AGCTCGCTGATCAGCCTCGACTGTGCCTTCTAGTTGCCAGCCATCTGTTGTTTGCCCT  
  
poly A  
1889 CCCCCGTGCCTTCCTTGACCCTGGAAGGTGCCACTCCCAGTGCCTTTCTAATAAAAT  
1948 GAGGAAATTGCATCGCATTGTCTGAGTAGGTGTCATTCTATTCTGGGGGGTGGGGTGGG  
2007 GCAGGACAGCAAGGGGGAGGATTGGGAAGACAATAGCAGGCATGCTGGGGATGCGGTGG  
2066 GCTCTATGGCTTCTGAGGCGGAAAGAACCAGTGGCGGTAATACGGTTATCCACAGAATC  
AflIII  
2125 AGGGGATAACGCAGGAAAGACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTA  
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Figure 1B (cont'd II)



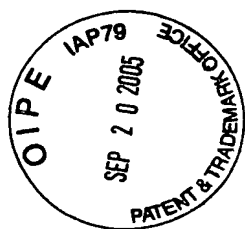
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2361 TGTCCGCCTTTCTCCCTTCGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTAT  
2420 CTCAGTTCGGTGTAGGTCGTTCCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCCGTTCA  
Col E1  
2479 GCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACG  
2538 ACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGC  
2597 GGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGGACAGTATT  
2656 TGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGAAAAAGAGTTGGTAGCTCTTGAT  
2715 CCGGCAAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGTGTTGCAAGCAGCAGATTACG  
2774 CGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGGTCTGACGCTCA  
2833 GTGGAACGAAAACCTCACGTTAAGGGATTTTGGTCATGAGATTATCAAAAAGGATCTTCA  
2892 CCTAGATCCTTTTAAATTAATAATGAAGTTTAAATCAATCTAAAGTATATATGAGTAA  
EcoO109I  
2951 CCTGAGGCTATGGCAGGGCCTGCCGCCCGACGTTGGCTGCGAGCCCTGGGCCTTCACC  
3010 CGAAGTTGGGGGTGGGGTGGGGAAAAGGAAGAAACGCGGGCGTATTGGCCCCAATGGG  
3069 GTCTCGGTGGGGTATCGACAGAGTGCCAGCCCTGGGACCGAACCCCGCGTTTATGAACA  
TK poly A  
3128 AACGACCCAACACCGTGCGTTTTATTCTGTCTTTTATTGCCGTCATAGCGCGGGTTCC  
3187 TTCCGGTATTGTCTCCTTCCGTGTTTCAGTTAGCCTCCCCCTAGGGTGGGCGAAGAACT  
3246 CCAGCATGAGATCCCCGCGCTGGAGGATCATCCAGCCGGCGTCCCGGAAAACGATTCCG  
3305 AAGCCCAACCTTTCATAGAAGGCGGCGGTGGAATCGAAATCTCGTGATGGCAGGTTGGG  
3364 CGTCGCTTGGTCGGTCATTTTGAACCCAGAGTCCCGCTCAGAAGAACTCGTCAAGAAG  
2634 ●●●PhePheGluAspLeuLeu  
3423 GCGATAGAAGGCGATGCGCTGCGAATCGGGAGCGGCGATACCGTAAAGCACGAGGAAGC  
2564 ArgTyrPheAlaIleArgGlnSerAspProAlaAlaIleGlyTyrLeuValLeuPheAr  
3482 GGTACGCCCATTCGCCGCCAAGCTCTTCAGCAATATCACGGGTAGCCAACGCTATGTCC  
2364 gAspAlaTrpGluGlyLeuGluAlaIleAspArgThrAlaLeuAlaIleAspG  
RsrII  
3541 TGATAGCGGTCCGCCACACCCAGCCGGCCACAGTCGATGAATCCAGAAAAGCGGCCATT  
2164 InTyrArgAspAlaValGlyLeuArgGlyCysAspIlePheGlySerPheArgGlyAsn  
3600 TTCCACCATGATATTCGGCAAGCAGGCATCGCCATGGGTACGACGAGATCCTCGCCGT  
1974 GluValMetIleAsnProLeuCysAlaAspGlyHisThrValValLeuAspGluGlyAs  
3659 CGGGCATGCTCGCCTTGAGCCTGGCGAACAGTTCGGCTGGCGCGAGCCCTGATGCTCT  
1774 pProMetSerAlaLysLeuArgAlaPheLeuGluAlaProAlaLeuGlyGlnHisGluG  
BclI

Figure 1B (cont'd III)



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3777 TTTGCTTGGTGGTGAATGGGAGGTAGCCGGATCAAGCGTATGCAGCCGCCGATTG  
1384 LysAlaGlnHisAspPheProCysThrAlaProAspLeuThrHisLeuArgArgMetAla  
3836 CATCAGCCATGATGGATACTTTCTCGGAGGAGCAAGGTGAGATGACAGGAGATCCTGC  
1184 aAspAlaMetIleSerValLysGluAlaProAlaLeuHisSerSerLeuLeuAspGlnG  
Tth1111 Pvull  
3895 CCCGGCACTTCGCCAATAGCAGCCAGTCCCTTCCCGCTTCAGTGACAACGTCGAGCAC  
984 IyProValGluGlyLeuLeuLeuTrpAspArgGlyAlaGluThrValValAspLeuVal  
Neo-R.  
FspI MscI  
3954 AGCTGCGCAAGGAACGCGCTCGTGGCCAGCCACGATAGCCGCGCTGCCTCGTCTTGCA  
794 AlaAlaCysProValGlyThrThrAlaLeuTrpSerLeuArgAlaAlaGluAspGlnLe  
NarI  
4013 GTTCATTCAGGGCACCGGACAGGTCTGACAAAAAGAACGGCGCCCTGCGCT  
594 uGluAsnLeuAlaGlySerLeuAspThrLysValPheLeuValProArgGlyGlnAlaS  
4072 GACAGCCGGAACACGGCGCATCAGAGCAGCCGATTGTCTGTTGTGCCAGTCATAGCC  
394 erLeuArgPheValAlaAlaAspSerCysGlyIleThrGlnGlnAlaTrpAspTyrGly  
4131 GAATAGCCTCTCCACCCAAGCGCGGAGAACCTGCGTGCAATCCATCTTGTTCATCA  
204 PheLeuArgGluValTrpAlaAlaProSerGlyAlaHisLeuGlyAspGlnGluIleMe  
BsaBI ClaI AvrII  
4190 TGCGAAACGATCCTCATCCTGTCTCTTGATCGATCTTTGCAAAAGCCTAGGCCTCCAAA  
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4308 CATAAATAAAAAAATTAGTCAGCCATGGGGCGGAGAATGGGCGGAACCTGGGCGGAGTT  
SV40 ori & Promotor NsiI  
4367 AGGGGCGGGATGGGCGGAGTTAGGGGCGGGACTATGGTTGCTGACTAATTGAGATGCAT  
SexAI  
4426 GCTTTGCATACTTCTGCCTGCTGGGGAGCCTGGGGACTTTCCACACCTGGTTGCTGACT  
NsiI  
4485 AATTGAGATGCATGCTTTGCATACTTCTGCCTGCTGGGGAGCCTGGGGACTTTCCACAC  
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4544 CCTAACTGACACACATTCCACAGCTGGTTCTTTCCGCCTCAGGACTCTTCCTTTTTCAA  
4603 TAAATCAATCTAAAGTATATATGAGTAACTTGGTCTGACAGTTACCAATGCTTAATCA  
2874 •••TrpHisLysIleLe  
Eam1105I  
4662 GTGAGGCACCTATCTCAGCGATCTGTCTATTTCTGTTTCATCCATAGTTGCCTGACTCCCC  
2814 uSerAlaGlyIleGluAlaIleGlnArgAsnArgGluAspMetThrAlaGlnSerGlyT  
4721 GTCGTGTAGATAACTACGATACGGGAGGCTTACCATCTGGCCCCAGTGCTGCAATGAT  
2614 hrThrTyrIleValValIleArgSerProLysGlyAspProGlyLeuAlaAlaIleIle  
4780 ACCGCGAGACCCACGCTCACCGGCTCCAGATTTATCAGCAATAAACCCAGCCAGCCGGAA  
2424 GlyArgSerGlyArgGluGlyAlaGlySerLysAspAlaIlePheTrpGlyAlaProLe  
4839 GGGCCGAGCGCAGAAGTGGTCTGCACTTTATCCGCCTCCATCCAGTCTATTAATTGT  
2224 uAlaSerArgLeuLeuProGlyAlaValLysAspAlaGluMetTrpAspIleLeuGlnG  
FspI Psp1406I  
4898 TGCCGGGAAGCTAGAGTAAGTAGTTCGCCAGTTAATAGTTTGCGCAACGTTGTTGCCAT  
2024 I nArgSerAlaLeuThrLeuLeuGluGlyThrLeuLeuLysArgLeuThrThrAlaMet  
4957 TGCTACAGGCATCGTGGTGTACGCTCGTCTTGGTATGGCTTCATTACGCTCCGGTT  
1834 AlaValProMetThrThrAspArgGluAspAsnProIleAlaGluAsnLeuGluProGlu

Figure 1B (cont'd IV)



5016 CCCAACGATCAAGGCGAGTTACATGATCCCCCATGTTGTGCAAAAAAGCGGTTAGCTCC  
 1634 uTrpArgAspLeuArgThrValHisAspGlyMetAsnHisLeuPheAlaThrLeuGluL  
 PvuI

5075 TTCGGTCTCCGATCGTTGTCAGAAGTAAGTTGGCCGCAGTGTTATCACTCATGGTTAT  
 1434 ysProGlyGlyIleThrThrLeuLeuLeuAsnAlaAlaThrAsnAspSerMetThrIle  
 bla

5134 GGCAGCACTGCATAAFTCTCTTACTGTCATGCCATCCGTAAGATGCTTTTCTGTGACTG  
 1244 AlaAlaSerCysLeuGluArgValThrMetGlyAspThrLeuHisLysGluThrValPr  
 ScaI

5193 GTGAGTACTCAACCAAGTCATTCTGAGAATAGTGTATGCGGCGACCGAGTTGCTCTTGC  
 1044 oSerTyrGluValLeuAspAsnGlnSerTyrHisIleArgArgGlyLeuGlnGluGlnG  
 5252 CCGGCGTCAATACGGGATAATACCGCGCCACATAGCAGAACTTTAAAAGTGCTCATCAT  
 844 IyAlaAspIleArgSerLeuValAlaGlyCysLeuLeuValLysPheThrSerMetMet  
 Psp1406I

5311 TGGAAAAACGTTCTTCGGGGCGAAAACTCTCAAGGATCTTACCGCTGTTGAGATCCAGTT  
 654 ProPheArgGluGluProArgPheSerGluLeuIleLysGlySerAsnLeuAspLeuGlu  
 ApaLI

5370 CGATGTAACCCACTCGTGCACCCAACTGATCTTCAGCATCTTTTACTTTCACCAGCGTT  
 454 ulleTyrGlyValArgAlaGlyLeuGlnAspGluAlaAspLysValLysValLeuThrG  
 5429 TCTGGGTGAGCAAAAACAGGAAGGCAAAATGCCGCAAAAAAGGGAAATAAGGGCGACACG  
 254 IuProHisAlaPheValProLeuCysPheAlaAlaPhePheProIleLeuAlaValArg  
 SspI

5488 GAAATGTTGAATACTCATACTCTTCCTTTTCAATATTATTGAAGCATTTATCAGGGT  
 64 PheHisGlnIleSerMet  
 BspHI

5547 ATTGTCTCATGAGCGGATACATATTTGAATGTATTTAGAAAAATAAACAAATAGGGGT  
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5665 GCGGGGTGTGGTGGTTACGCGCAGCGTGACCGCTACACTTGCCAGCGCCCTAGCGCCCC

5724 CTCCTTTCGCTTTCTTCCTTCTCTTCGCCACGTTGCGCGGCTTTCCCCGTCAAGCT

5783 CTAAATCGGGGGCTCCCTTTAGGGTTCCGATTTAGTGCTTTACGGCACCTCGACCCCAA

5842 AAAACTTGATTAGGGTGATGGTTCACGTAGTGGGCCATCGCCCTGATAGACGGTTTTTC

5901 GCCCTTTGACGTTGGAGTCCACGTTCTTTAATAGTGGACTCTTGTTCCAAACTGGAACA

5960 ACACTCAACCCATCTCGGTCTATTCTTTGATTTATAAGGGATTTTGCCGATTTCCGGC

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6078 TAACGCTTACAATTTAC

Figure 1B (cont'd V)

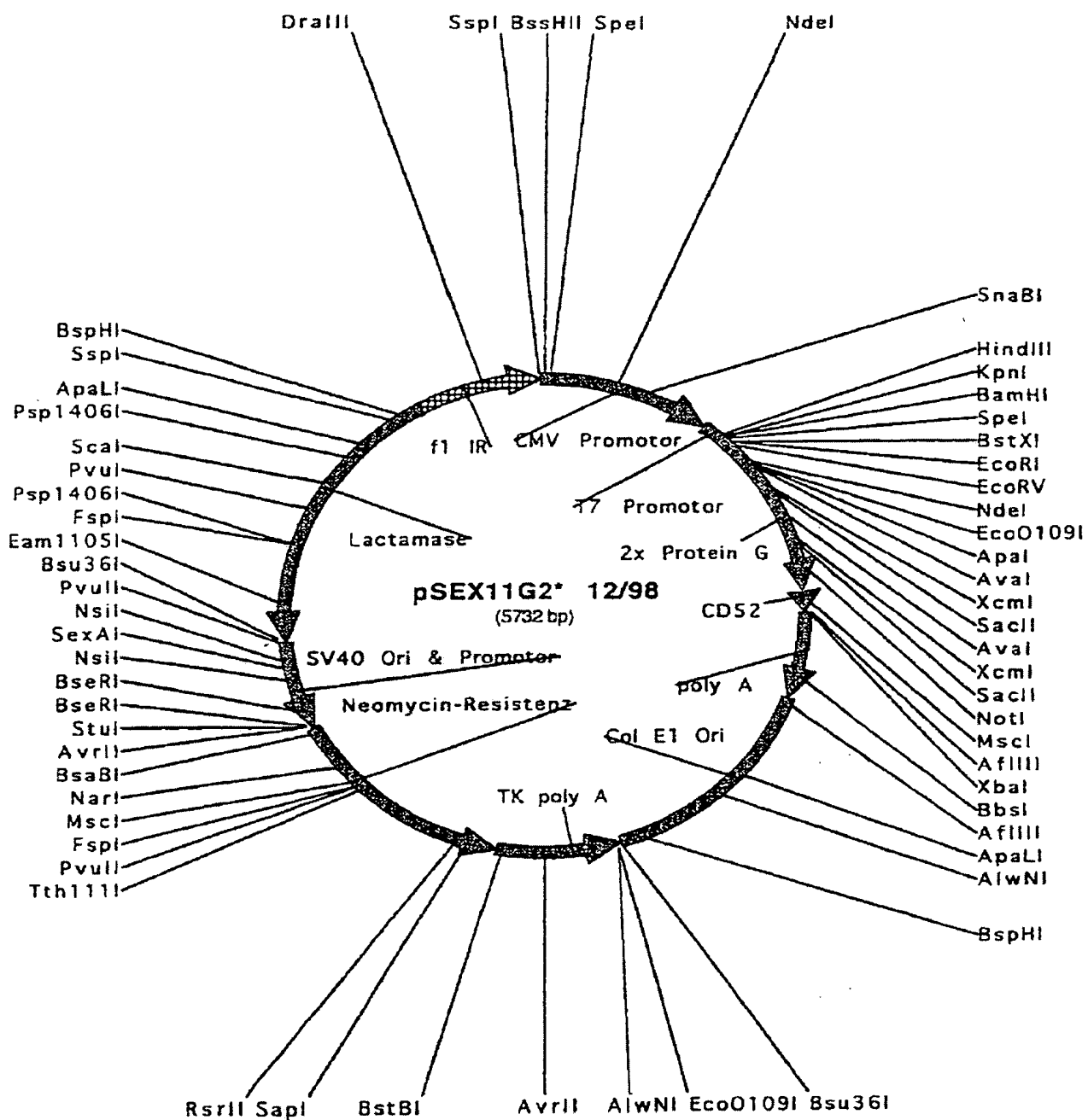
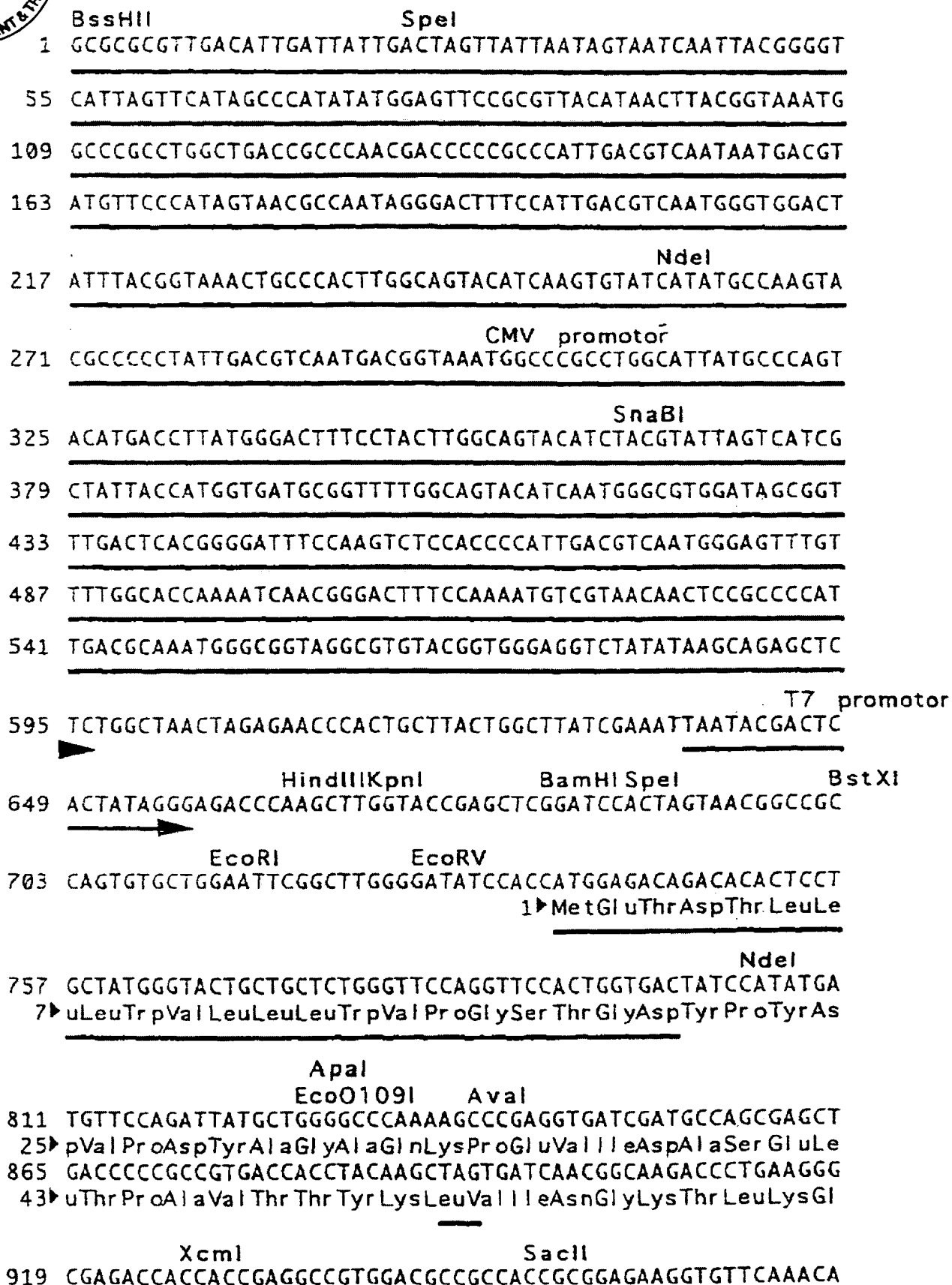
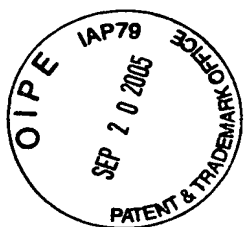


Figure 2 A



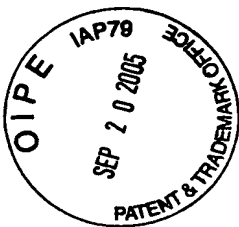
### Figure 2B (cont'd I)





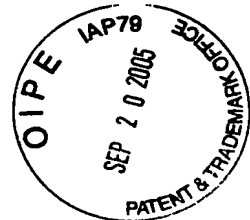
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79 nTyrAlaAsnAspAsnGlyValAspGlyGluTrpThrTyrAspAspAlaThrLy  
Aval  
2x Protein G  
1027 GACCTTCACCGTGACCGAGAAGCCCGAGGTGATCGATGCCAGCGAGCTGACCCC  
97 sThrPheThrValThrGluLysProGluVallleAspAlaSerGluLeuThrPr  
1081 CGCCGTGACCACCTACAAGCTAGTGATCAACGGCAAGACCCTGAAGGGCGAGAC  
115 oAlaValThrThrTyrLysLeuVallleAsnGlyLysThrLeuLysGlyGluTh  
XcmI SacII  
1135 CACCACCGAGGCCGTGGACGCCGCCACCGGAGAAGGTGTTCAAACAATACGC  
133 rThrThrGluAlaValAspAlaAlaThrAlaGluLysValPheLysGluTyrAl  
1189 TAATGACAACGGGGTCGACGGCGAGTGGACTTACGACGACGCCACCAAGACCTT  
151 aAsnAspAsnGlyValAspGlyGluTrpThrTyrAspAspAlaThrLysThrPh  
NotI  
1243 CACCGTGACCGAGGCGGCCGAGAACAAAACTCATCTCAGAAGAGGATCTGAA  
169 eThrValThrGluAlaAlaAlaGluLysLeulleSerGluGluAspLeuAs  
1297 TGGGGCCGTGACGGACAAAACGACACCAGCCAAACCAGCAGCCCCCTCAGCATC  
187 nGlyAlaValAspGlyGluAsnAspThrSerGluThrSerSerProSerAlaSe  
CD52 MscI  
1351 CAGCAACATAAGCGGAGGCATTTTCCTTTTCTTCGTGGCCAATGCCATAATCCA  
205 rSerAsnilleSerGlyGlyllePheLeuPhePheValAlaAsnAlallelleHi  
AflIII XbaI  
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223 sLeuPheCysPheSer...  
1459 AAATGCTAGAGCTCGCTGATCAGCCTCGACTGTGCCTTCTAGTTGCCAGCCATC  
1513 TGTTGTTTGGCCCTCCCCGTGCCTTCCTTGACCCTGGAAGGTGCCACTCCCAC  
poly A  
1567 TGTCCTTTCTAATAAAATGAGGAAATTGCATCGCATTGTCTGAGTAGGTGTCA  
BbsI  
1621 TTCTATTCTGGGGGGTGGGGTGGGGCAGGACAGCAAGGGGGAGGATTGGGAAGA  
1675 CAATAGCAGGCATGCTGGGGATGCGGTGGGCTCTATGGCTTCTGAGGCGGAAAG  
1729 AACCAGTGGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGA  
AflIII  
1783 ACATGTGAGCAAAAAGGCCAGCAAAAAGGCCAGGAACCGTAAAAAGGCCCGCTTGC  
1837 TGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAATCGACGCT  
1891 CAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCC

Figure 2B (cont'd II)



1945 CTGGAAGCTCCCTCGTGCGCTCTCCTGTTCCGACCCTGCCGCTTACCGGATACC  
1999 TGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTA  
2053 GGTATCTCAGTTCGGTGTAGGTCGTTTCGCTCCAAGCTGGGCTGTGTGCACGAAC  
2107 CCCCCGTTTCAGCCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCA  
2161 ACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTA  
2215 GCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACT  
2269 ACGGCTACACTAGAAGGACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTA  
2323 CCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTA  
2377 GCGGTGGTTTTTTTTGTTTGCAAGCAGCAGATTACGCGCAGAAAAAAGGATCTC  
2431 AAGAAGATCCTTTGATCTTTTCTACGGGGTCTGACGCTCAGTGGAAACGAAAAC  
2485 CACGTTAAGGGATTTTGGTCATGAGATTATCAAAAAGGATCTTCACCTAGATCC  
2539 TTTTAAATTAATAATGAAGTTTTAAATCAATCTAAAGTATATATGAGTAACCTG  
2593 AGGCTATGGCAGGGCCTGCCGCCCCGACGTTGGCTGCGAGCCCTGGGCCTTCAC  
2647 CCGAACTTGGGGGTGGGGTGGGGAAAAGGAAGAAACGCGGGCGTATTGGCCCC  
2701 AATGGGGTCTCGGTGGGGTATCGACAGAGTGCCAGCCCTGGGACCGAACCCCGC  
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3079 CTGCGAATCGGGAGCGGCGATACCGTAAAGCACGAGGAAGCGGTACGCCATTCC  
2504 GlnSerAspProAlaAlaIleGlyTyrLeuValLeuPheArgAspAlaTrpGlu  
SapI RsrII

Figure 2B (cont'd III)



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2324 GlyGlyLeuGluGluAlaIleAspArgThrAlaLeuAlaIleAspGlnTyrArg  
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2144 AspAlaValGlyLeuArgGlyCysAspIlePheGlySerPheArgGlyAsnGlu  
3241 CACCATGATATTCGGCAAGCAGGCATCGCCATGGGTACGACGAGATCCTCGCC  
1964 ValMetIleAsnProLeuCysAlaAspGlyHisThrValValLeuAspGluGly  
3295 GTCCGGCATGCTCGCCTTGAGCCTGGCGAACAGTTCGGCTGGCGCGAGCCCTG  
1784 AspProMetSerAlaLysLeuArgAlaPheLeuGluAlaProAlaLeuGlyGln  
3349 ATGCTCTTGATCATCCTGATCGACAAGACCGGCTTCCATCCGAGTACGTGCTCG  
1604 HisGluGlnAspAspGlnAspValLeuGlyAlaGluMetArgThrArgAlaArg  
3403 CTCGATGCGATGTTTCGCTTGGTGGTGAATGGGCAGGTAGCCGGATCAAGCGT  
1424 GluIleArgHisLysAlaGlnHisAspPheProCysThrAlaProAspLeuThr  
3457 ATGCAGCCGCCGATTGCATCAGCCATGATGGATACTTTCTCGGCAGGAGCAAG  
1244 HisLeuArgArgMetAlaAspAlaMetIleSerValLysGluAlaProAlaLeu  
3511 GTGAGATGACAGGAGATCCTGCCCCGGCACTTCGCCCAATAGCAGCCAGTCCCT  
1064 HisSerSerLeuLeuAspGlnGlyProValGluGlyLeuLeuLeuTrpAspArg

FspI

Neo-R.

Tth1111

PvuII

MscI

3565 TCCCGCTTCAGTGACAACGTGAGCACAGCTGCGCAAGGAACGCCCGTCGTGGC  
884 GlyAlaGluThrValValAspLeuValAlaAlaCysProValGlyThrThrAla  
3619 CAGCCACGATAGCCGCGCTGCCTCGTCTTGCAAGTTCATTCAGGGCACCGGACAG  
704 LeuTrpSerLeuArgAlaAlaGluAspGlnLeuGluAsnLeuAlaGlySerLeu

NarI

3673 GTCGGTCTTGACAAAAAGAACCGGGCGCCCTGCGCTGACAGCCGGAACACGGC  
524 AspThrLysValPheLeuValProArgGlyGlnAlaSerLeuArgPheValAla  
3727 GGCATCAGAGCAGCCGATTGTCTGTTGTGCCAGTCATAGCCGAATAGCCTCTC  
344 AlaAspSerCysGlyIleThrGlnGlnAlaTrpAspTyrGlyPheLeuArgGlu  
3781 CACCCAAGCGGCGGAGAACCTGCGTGCAATCCATCTTGTTCATCATGCGAAA  
164 ValTrpAlaAlaProSerGlyAlaHisLeuGlyAspGlnGluIleMet

StuI

BsaBI

AvrII

3835 CGATCCTCATCCTGTCTCTTGATCGATCTTTGCAAAAGCCTAGGCCTCCAAAAA

BseRI

BseRI

3889 AGCCTCCTCACTACTTCTGGAATAGCTCAGAGGCCGAGGAGGCGGCCTCGGCCT

3943 CTGCATAAATAAAAAAATTAGTCAGCCATGGGGCGGAGAAATGGGCGGAACTGG

SV40 ori & Promotor

3997 GCGGAGTTAGGGGCGGGATGGGCGGAGTTAGGGGCGGGACTATGGTTGCTGACT

NsiI

4051 AATTGAGATGCATGCTTTGCATACTTCTGCCTGCTGGGGAGCCTGGGGACTTTC

SexAI

NsiI

4105 CACACCTGGTTGCTGACTAATTGAGATGCATGCTTTGCATACTTCTGCCTGCTG

PvuII

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Bsu36I

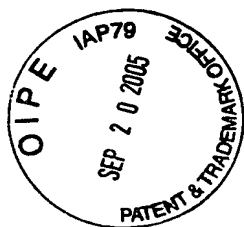
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4267 AAACCTGGTCTGACAGTTACCAATGCTTAATCAGTGAGGCACCTATCTCAGCGA

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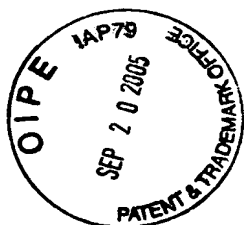
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Figure 2B (cont'd IV)



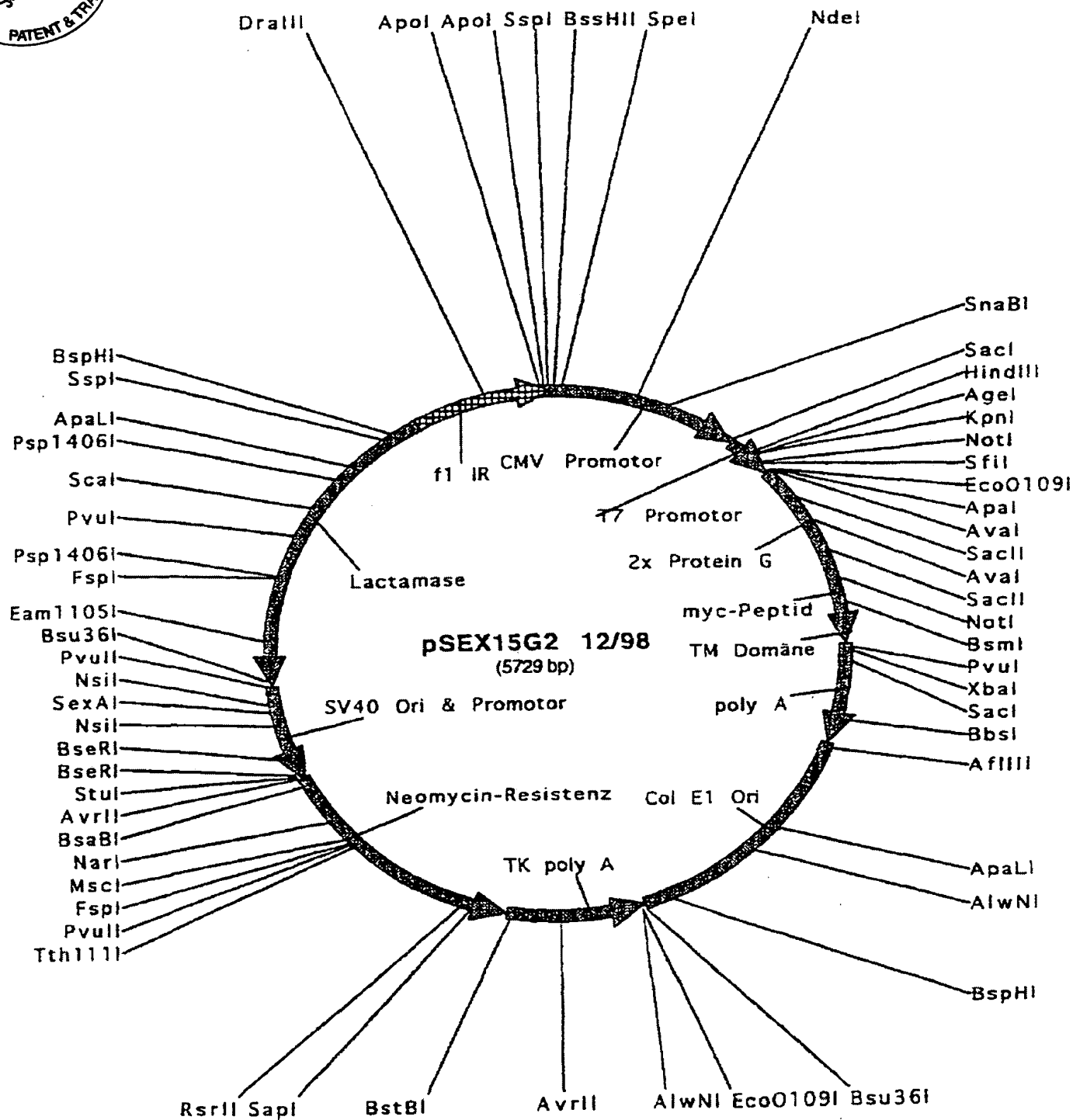
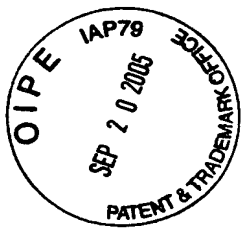
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274 eGlnArgAsnArgGluAspMetThrAlaGlnSerGlyThrThrTyrIleValVa  
4375 CGATACGGGAGGGCTTACCATCTGGCCCCAGTGCTGCAATGATACCGCGAGACC  
256 lllleArgSerProLysGlyAspProGlyLeuAlaAlallelleGlyArgSerGl  
4429 CACGCTCACCGGCTCCAGATTATCAGCAATAAACAGCCAGCCGGAAGGGCCG  
238 yArgGluGlyAlaGlySerLysAspAlallePheTrpGlyAlaProLeuAlaSe  
4483 AGCGCAGAAGTGGTCCTGCAACTTTATCCGCCTCCATCCAGTCTATTAATTGTT  
220 rArgLeuLeuProGlyAlaValLysAspAlaGluMetTrpAspilleLeuGlnGl  
FspI Psp1406I  
4537 GCCGGGAAGCTAGAGTAAGTAGTTCGCCAGTTAATAGTTTGCGCAACGTTGTTG  
202 nArgSerAlaLeuThrLeuLeuGluGlyThrLeuLeuLysArgLeuThrThrAl  
4591 CCATTGCTACAGGCATCGTGGTGTACGCTCGTCGTTTGGTATGGCTTCATTCA  
184 aMetAlaValProMetThrThrAspArgGluAspAsnProilleAlaGluAsnLe  
4645 GCTCCGGTTCCCAACGATCAAGGCGAGTTACATGATCCCCATGTTGTGCAAAA  
166 uGluProGluTrpArgAspLeuArgThrValHisAspGlyMetAsnHisLeuPh  
PvuI  
4699 AAGCGGTTAGCTCCTTCGGTCCTCCGATCGTTGTCAGAAGTAAGTTGGCCGCAG  
148 eAlaThrLeuGluLysProGlyGlyilleThrThrLeuLeuLeuAsnAlaAlaTh  
4753 TGTTATCACTCATGGTTATGGCAGCACTGCATAATTCTCTTACTGTCATGCCAT  
130 rAsnAspSerMetThrilleAlaAlaSerCysLeuGluArgValThrMetGlyAs  
bla Scal  
4807 CCGTAAGATGCTTTTCTGTGACTGGTGAGTACTCAACCAAGTCATTCTGAGAAT  
112 pThrLeuHisLysGluThrValProSerTyrGluValLeuAspAsnGlnSerTy  
4861 AGTGTATGCGGCGACCGAGTTGCTCTTGCCCGCGTCAATACGGGATAATACCG  
94 rHisilleArgArgGlyLeuGlnGluGlnGlyAlaAspilleArgSerLeuValAl  
Psp1406I  
4915 CGCCACATAGCAGAACTTTAAAAGTGCTCATCATTGGAAAACGTTCTTCGGGGC  
76 aGlyCysLeuLeuValLysPheThrSerMetMetProPheArgGluGluProAr  
4969 GAAAACTCTCAAGGATCTTACCGCTGTTGAGATCCAGTTCGATGTAACCCACTC  
58 gPheSerGluLeuilleLysGlySerAsnLeuAspLeuGluilleTyrGlyValAr  
ApaI  
5023 GTGCACCAACTGATCTTCAGCATCTTTTACTTTTACCAGCGTTTCTGGGTGAG  
40 gAlaGlyLeuGlnAspGluAlaAspLysValLysValLeuThrGluProHisAl  
5077 CAAAAACAGGAAGGCAAAATGCCGCAAAAAAGGAATAAGGGCGACACGGAAAT  
22 aPheValProLeuCysPheAlaAlaPhePheProilleLeuAlaValArgPheHi  
SspI  
5131 GTTGAATACTCATACTCTTCCTTTTTCAATATTATTGAAGCATTATCAGGGTT  
4 sGlnilleSerMet  
BspHI  
5185 ATTGTCTCATGAGCGGATACATATTTGAATGTATTTAGAAAAATAAACAAATAG  
5239 GGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCTGACGCGCCCTGTAGCGGCG  
Stem loop A  
5293 CATTAAGCGCGGCGGGTGTGGTGGTTACGCGCAGCGTGACCGCTACACTTGCCA  
5347 GCGCCCTAGCGCCCGCTCCTTTGCTTTCTTCCCTTCCTTTCTCGCCACGTTGCG  
f1 IR Stem loop B  
5401 CCGGCTTTCCCCGTCAAGCTCTAAATCGGGGGCTCCCTTTAGGGTTCCGATTTA

Figure 2B (cont'd V)



5455 GTGCTTTACGGCACCTCGACCCCAAAAACTTGATTAGGGTGATGGTTCACGTA **DraIII**  
\_\_\_\_\_  
\_\_\_\_\_  
5509 GTGGGCCATCGCCCTGATAGACGGTTTTTCGCCCTTTGACGTTGGAGTCCACGT **Start Transcription**  
                    **Stem loop C**                    **Primer-RNA**                    **VS-Synthese**  
\_\_\_\_\_  
\_\_\_\_\_  
5563 TCTTTAATAGTGGACTCTTGTTCCAACTGGAACAACACTCAACCCTATCTCGG  
                    **Nicking site** **Stem loop D**                    **Stem loop E**  
\_\_\_\_\_  
5617 TCTATTCTTTTGATTTATAAGGGATTTTGCCGATTCGGCCTATTGGTTAAAAA  
\_\_\_\_\_  
5671 ATGAGCTGATTTAACAAAAATTTAACGCGAATTTTAACAAAATATTAACGCTTA **SspI**  
\_\_\_\_\_  
5725 CAATTTAC

**Figure 2B (cont'd VI)**



**Figure 3 A**

**BssHII**

1 GCGCGCGTTGACATTGATTATTGACTAGTTATTAATAGTAATCAATTACGGGGTCA

**SpeI**

57 TTAGTTCATAGCCCATATATGGAGTTCGCGTTACATAACTTACGGTAAATGGCCC

113 GCCTGGCTGACCGCCCCAACGACCCCCGCCATTGACGTCAATAATGACGTATGTTCC

169 CCATAGTAACGCCAATAGGGACTTTCCATTGACGTCAATGGGTGGACTATTTACGG

**NdeI**

225 TAAACTGCCCACTTGCCAGTACATCAAGTGTATCATATGCCAAGTACGCCCCCTAT

**CMV promoter**

281 TGACGTCAATGACGGTAAATGGCCCGCCTGGCATTATGCCAGTACATGACCTTAT

**SnaBI**

337 GGGACTTTCCTACTTGGCAGTACATCTACGTATTAGTCATCGCTATTACCATGGTG

393 ATGCGGTTTTGGCAGTACATCAATGGGCGTGGATAGCGGTTTGACTCACGGGGATT

449 TCCAAGTCTCCACCCCATTGACGTCAATGGGAGTTTGTTTTGGCACCAAATCAAC

505 GGGACTTTCCAAATGTCGTAACAACCTCCGCCCCATTGACGCAAATGGGCGGTAGG

**SacI**

561 CGTGTACGGTGGGAGGTCTATATAAGCAGAGCTCTCTGGCTAACTAGAGAACCAC

**T7 promoter**

617 TGCTTACTGGCTTATCGAAATTAATACGACTCACTATAGGGAGACCCAAGCTTGGT

**HindIII KpnI**

**SfiI**

**AgeI**

673 ACCGGTGGCGATGGCACCCCTGCATGCTGCTCCTGCTGTTGGCGGGCCCTGGCCCC

1►MetAlaProCysMetLeuLeuLeuLeuAlaAlaAlaLeuAlaPr

**ApaI**

**EcoO109I**

**AvaI**

729 GACTCAGACCCGCGCGGGGGCCCCAAAAGCCCCGAGGTGATCGATGCCAGCGAGCTGA

16►oThrGlnThrArgAlaGlyAlaGlnLysProGluValIleAspAlaSerGluLeuT

785 CCCCCGCGGTGACCACCTACAAGCTAGTGATCAACGGCAAGACCCTGAAGGGCGAG

35►hrProAlaValThrThrTyrLysLeuValIleAsnGlyLysThrLeuLysGlyGlu

**SacII**

841 ACCACCACCGAGGCCGTGGACGCCGCCACCGCGGAGAAGGTGTTCAAACAATACGC

54►ThrThrThrGluAlaValAspAlaAlaThrAlaGluLysValPheLysGlnTyrAl

897 TAATGACAACGGGGTCGACGGCGAGTGGACTTACGACGACGCCACCAAGACCTTCA

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**AvaI**

**2x Protein G**

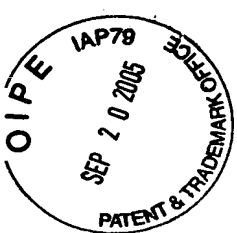
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1009 ACCTACAAGCTAGTGATCAACGGCAAGACCCTGAAGGGCGAGACCACCACCGAGGC

110►ThrTyrLysLeuValIleAsnGlyLysThrLeuLysGlyGluThrThrThrGluAl

### Figure 3B (cont'd I)



SacII

1065 CGTGGACGCCGCCACCGCGGAGAAGGTGTTCAAACAATACGCTAATGACAACGGGG  
128▶ aValAspAlaAlaThrAlaGluLysValPheLysGlnTyrAlaAsnAspAsnGlyV  
NotI

1121 TCGACGGCGAGTGGACTTACGACGACGCCACCAAGACCTTCACCGTGACCGAGGCG  
147▶ alAspGlyGluTrpThrTyrAspAspAlaThrLysThrPheThrValThrGluAla  
myc

1177 GCCGCAGAACAAAACTCATCTCAGAAGAGGATCTGAATGGGGCCGTCGACGAACA  
166▶ AlalaGluGlnLysLeuIleSerGluGluAspLeuAsnGlyAlaValAspGluGlu

BsmI

1233 AAAACTCATCTCAGAAGAGGATCTGAATGCTGTGGGCCAGGACACGCAGGAGGTCA  
184▶ nLysLeuIleSerGluGluAspLeuAsnAlaValGlyGlnAspThrGlnGluValI

1289 TCGTGGTGCCCACTCCTTGCCCTTTAAGGTGGTGGTGATCTCAGCCATCCTGGCC  
203▶ leValValProHisSerLeuProPheLysValValValIleSerAlaIleLeuAla

TM domain

1345 CTGGTGGTGCTCACCATCATCTCCCTTATCATCCTCATCATGCTTTGGCAGAAGAA  
222▶ LeuValValLeuThrIleIleSerLeuIleIleLeuIleMetLeuTrpGlnLysLy

PvuI                      XbaI

1401 GCCACGTTCTGTCGGCCGATCGAGAATCCATCTAGAGCTATTCTATAGTGTCACCTA  
240▶ sProArgSerSerAlaAspArgGluSerIle... — ←

SacI

1457 AATGCTAGAGCTCGCTGATCAGCCTCGACTGTGCCTTCTAGTTGCCAGCCATCTGT  
←

poly A

1513 TGTTTGCCCCCTCCCCCGTGCCTTCCTTGACCCTGGAAGGTGCCACTCCCACTGTCC  
1569 TTTCCTAATAAAATGAGGAAATTGCATCGCATTGTCTGAGTAGGTGTCATTCTATT

BbsI

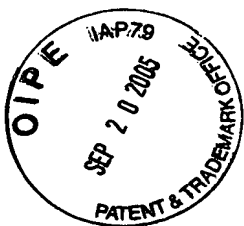
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1681 GCATGCTGGGGATGCGGTGGGCTCTATGGCTTCTGAGGCGGAAAGAACCAGTGGCG

AflIII

1737 GTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGAACATGTGAGCAAA  
1793 AGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTCCATA  
1849 GGCTCCGCCCCCTGACGAGCATCAGAAAAATCGACGCTCAAGTCAGAGGTGGCGA  
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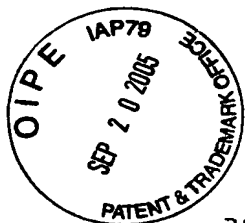
Figure 3B (cont'd II)





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2073 GTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCGTTGAGCCGACCGCTGCGC  
2129 CTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCAC  
2185 TGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACA  
2241 GAGTTCCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGGACAGTATTTGGTAT  
2297 CTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCG  
2353 GCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTTGTTTGCAAGCAGCAGATTACG  
2409 CGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGGTCTGACGC  
2465 TCAGTGGAACGAAAACCTCACGTTAAGGGATTTTGGTCATGAGATTATCAAAAAGGA  
2521 TCTTCACCTAGATCCTTTTAAATTAATAATGAAGTTTTAAATCAATCTAAAGTATA  
2577 TATGAGTAACCTGAGGCTATGGCAGGGCCTGCCGCCCCGACGTTGGCTGCGAGCCC  
2633 TGGGCCTTCACCCGAACCTTGGGGGTGGGGTGGGGAAAAGGAAGAAACGCGGGCGT  
2689 ATTGGCCCCAATGGGGTCTCGGTGGGGTATCGACAGAGTGCCAGCCCTGGGACCGA  
2745 ACCCCGCGTTTATGAACAAACGACCCAACACCGTGCGTTTTATTCTGTCTTTTTAT  
2801 TGCCGTCATAGCGCGGGTTCCTTCCGGTATTGTCTCCTTCCGTGTTTCAGTTAGCC  
2857 TCCCCCTAGGGTGGGCGAAGAACTCCAGCATGAGATCCCCGEGCTGGAGGATCATC  
2913 CAGCCGGCGTCCCGGAAAACGATTCCGAAGCCCAACCTTTCATAGAAGGCGGCGGT  
2969 GGAATCGAAATCTCGTGATGGCAGGTTGGGCGTCGCTTGGTCGGTCATTTTCAAAAC  
3025 CCAGAGTCCCGCTCAGAAGAACTCGTCAAGAAGGCGATAGAAGGCGATGCGCTGCG  
2634 ●●●PhePheGluAspLeuLeuArgTyrPheAlaIleArgGlnSer  
3081 AATCGGGAGCGGCGATACCGTAAAGCACGAGGAAGCGGTGAGCCCATTCGCCGCCA  
2484 rAspProAlaAlaIleGlyTyrLeuValLeuPheArgAspAlaTrpGluGlyGlyL  
3137 AGCTCTTCAGCAATATCACGGGTAGCCAACGCTATGTCCTGATAGCGGTCCGCCAC  
2294 euGluGluAlaIleAspArgThrAlaLeuAlaIleAspGlnTyrArgAspAlaVal  
3193 ACCCAGCCGGCCACAGTCGATGAATCCAGAAAAGCGGCCATTTCCACCATGATAT  
2114 GlyLeuArgGlyCysAspIlePheGlySerPheArgGlyAsnGluValMetIleAs  
3249 TCGGCAAGCAGGCATCGCCATGGGTACGACGAGATCCTCGCCGTGGGCATGCTC  
1924 nProLeuCysAlaAspGlyHisThrValValLeuAspGluGlyAspProMetSerA  
3305 GCCTTGAGCCTGGCGAACAGTTCGGCTGGCGCGAGCCCCTGATGCTCTTGATCATC  
1734 lalaLysLeuArgAlaPheLeuGluAlaProAlaLeuGlyGlnHisGluGluAspAsp

Figure 3B (cont'd III)



3921 BseRI  
GAGGAGGCGGCCTCGGCCTCTGCATAAATAAAAAAATTAGTCAGCCATGGGGCGG

3977 SV40 ori & Promotor  
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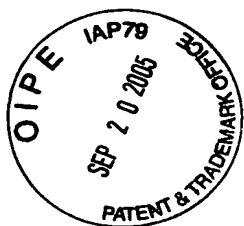
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4089 SexAI NsiI  
CCTGGGGACTTTCCACACCTGGTTGCTGACTAATTGAGATGCATGCTTTGCATACT

4145 Pvull  
TCTGCCTGCTGGGGAGCCTGGGGACTTTCCACACCCTAACTGACACACATTCCACA

4201 Bsu36I  
GCTGGTTCTTTCCGCCTCAGGACTCTTCCTTTTCAATAAAICAATCTAAAGTATA  
4257 TATGAGTAACTTGGTCTGACAGTTACCAATGCTTAATCAGTGAGGCACCTATCTC  
2874 ●●●TrpHisLysIleLeuSerAlaGlyIleGlu  
Eam1105I  
3361 CTGATCGACAAGACCGGCTTCCATCCGAGTACGTGCTCGCTCGATGCGATGTTTCG  
1554 Gl nAspValLeuGlyAlaGluMetArgThrArgAlaArgGluIleArgHisLysAl  
3417 CTTGGTGGTGAATGGGCGGAGTACCGGATCAAGCGTATGCAGCCGCCGATTGCA  
1364 aGlnHisAspPheProCysThrAlaProAspLeuThrHisLeuArgArgMetAlaA  
3473 TCAGCCATGATGGATACTTTCTCGGCAGGAGCAAGGTGAGATGACAGGAGATCCTG  
1174 spAlaMetIleSerValLysGluAlaProAlaLeuHisSerSerLeuLeuAspGln  
Tth111I  
3529 CCCC GGCACTTCGCCCCAATAGCAGCCAGTCCCTTCCCGCTTCAGTGACAACGTGCA  
994 GlyProValGluGlyLeuLeuLeuTrpAspArgGlyAlaGluThrValValAspLe  
Neo-R.  
PvullFspI MscI  
3585 GCACAGCTGCGCAAGGAACGCCCGTCGTGGCCAGCCACGATAGCCGCGCTGCCTCG  
804 uValAlaAlaCysProValGlyThrThrAlaLeuTrpSerLeuArgAlaAlaGluA  
NarI  
3641 TCTTGCAGTTCATTACAGGGCACCGGACAGGTCTTGTGACAAAAGAACCGGGCGG  
614 spGlnLeuGluAsnLeuAlaGlySerLeuAspThrLysValPheLeuValProArg  
3697 CCCCTGCGCTGACAGCCGGAACACGGCGGCATCAGAGCAGCCGATTGTCTGTTGTG  
434 GlyGlnAlaSerLeuArgPheValAlaAlaAspSerCysGlyIleThrGlnGlnAl  
3753 CCCAGTCATAGCCGAATAGCCTCTCCACCCAAGCGGCCGAGAACCTGCGTGCAAT  
244 aTrpAspTyrGlyPheLeuArgGluValTrpAlaAlaProSerGlyAlaHisLeuG  
BsaBI  
3809 CCATCTTGTTCATCATGCGAAACGATCCTCATCCTGTCTCTTGATCGATCTTTGC  
54 IyAspGlnGluIleMet  
StuI  
AvrII BseRI  
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Figure 3B (cont'd IV)



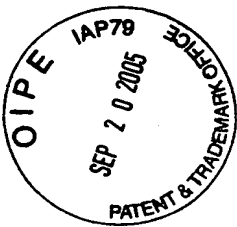
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FspI Psp1406I  
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1644GluTrpArgAspLeuArgThrValHisAspGlyMetAsnHisLeuPheAlaThrLe  
PvuI  
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bla  
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ScaI  
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4873 CGAGTTGCTCTTGGCCGGCGTCAATACGGGATAATACCGCGCCACATAGCAGAACT  
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ApaLI  
4985 ACCGCTGTTGAGATCCAGTTCGATGTAACCCACTCGTGCAACCAACTGATCTTCAG  
524GlySerAsnLeuAspLeuGluIleTyrGlyValArgAlaGlyLeuGlnAspGluAl  
5041 CATCTTTTACTTTCCACCAGCGTTTCTGGGTGAGCAAAAACAGGAAGGCAAAATGCC  
334aAspLysValLysValLeuThrGluProHisAlaPheValProLeuCysPheAlaA  
5097 GCAAAAAAGGGAATAAGGGCGACACGGAAATGTTGAATACTCATACTCTTCCTTTT  
144IaPhePheProIleLeuAlaValArgPheHisGlnIleSerMet  
SspI BspHI  
5153 TCAATATTATTGAAGCATTATCAGGGTTATTGTCTCATGAGCGGATACATATTTG  
5209 AATGTATTTAGAAAAATAAACAAATAGGGGTTCCGCGCACATTTCCCCGAAAAGTG  
5265 CCACCTGACGCGCCCTGTAGCGGCGCATTAAGCGCGGCGGGTGTGGTGGTTACGCG

Stem loop A

5321 CAGCGTGACCGCTACACTTGCCAGCGCCCTAGCGCCCGCTCCTTTTCGCTTTCTTCC

5377 CTTCTTTTCTCGCCACGTTCCGCGGCTTTCCCCGTCAAGCTCTAAATCGGGGGCTC

Figure 3B (cont'd V)



5433 f1 IR Stem loop B  
CCTTTAGGGTTCGATTAGTGCTTTACGGCACCTCGACCCCAAAAACTTGATTA

---

5489 Dralll Stem loop C Primer-RNA  
GGGTGATGGTTCACGTAGTGGGCCATCGCCCTGATAGACGGTTTTTCGCCCTTGA

---

5545 Start Transcription  
VS-Synthese Nicking site Stem loop D Stem loop E  
CGTTGGAGTCCACGTTCTTTAATAGTGGACTCTTGTTCCAACTGGAACAACACTC

---

5601 AACCTATCTCGGTCTATTCTTTGATTTATAAGGGATTTTGCCGATTTCGGCCTA

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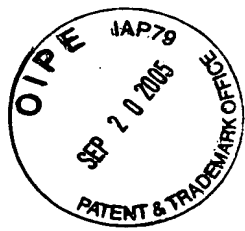
5657 Apol Apol Sspl  
TTGGTTAAAAAATGAGCTGATTTAACAAAAATTTAACGCGAATTTTAACAAAATAT

---

5713 TAACGCTTACAATTTAC

---

Figure 3B (cont'd VI)



f1 IR                      Stem loop B  
5433 CCTTTAGGGTTCCGATTTAGTGCTTTACGGCACCTCGACCCCAAAAACTTGATTA  
\_\_\_\_\_

Dralll                      Stem loop C                      Primer-RNA  
5489 GGGTGATGGTTCACGTAGTGGGCCATCGCCCTGATAGACGGTTTTTCGCCCTTTGA  
\_\_\_\_\_

Start Transcription  
VS-Synthese Nicking site   Stem loop D                      Stem loop E  
5545 CGTTGGAGTCCACGTTCTTTAATAGTGGACTCTTGTTCCAAACTGGAACAACACTC  
\_\_\_\_\_

5601 AACCTATCTCGGTCTATTCTTTTGATTTATAAGGGATTTTGCCGATTTCGGCCTA  
\_\_\_\_\_

   Apol                      Apol                      Sspl  
5657 TTGGTAAAAAATGAGCTGATTTAACAAAAATTTAACGCGAATTTTAACAAAATAT  
\_\_\_\_\_

5713 TAACGCTTACAATTTAC  
\_\_\_\_\_

**Figure 3B (cont'd VI)**